

FIG.1

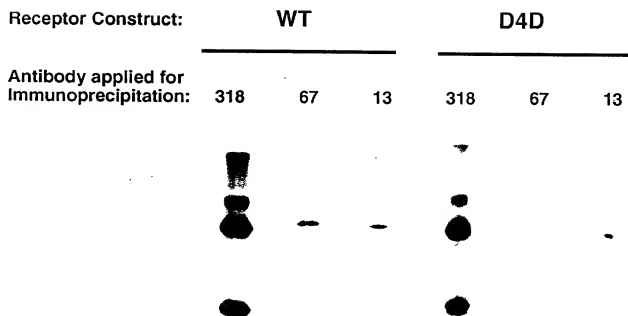


FIG. 2A

1 gcgagcgacg cggagcctgg agagagcgg ctgggctgag ggcgcgaggg cagggggcaa cgggaccccg
81 ccgcaccc atg gcg ccc gtc gtc tgg gcc gcg ctg gtc gga ctg gag etc tgg gct gcg
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
-22
147 gcg cac gtc ccc gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg
Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
213 -1 +1
ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tgc ccg ggc caa cat gca
Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala
279.
aaa gtc ttc tgt acc aag acc tgc gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag
Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
345.
etc tgg aac tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act
Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
411.
caa gcc tgc act cgg gaa cag aac cgc atc tgc acd tgc agc tcc ggc tgg tac tgc gcg ctg agc
Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
477.
aag cag gag ggg tgc cgg ctg tgc gcg ccg ctg cgc aag tgc agc ccg ggc ttc ggc gtg gcc aga
Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg
543.
cca gga act gaa aca tca gac gtg tgc aag ccc tgt gcc ccc ggg acg ttc ttc aac acg act
Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr
609.
tca tcc acg gat act tgc aga ccc cag atc tgc aac gtg gtg gcc atc ccc ggg aat gca agc
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
675.
atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cag tta ccc
Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro
741.
120
142
164
186

TBP11

FIG. 2B

cag cca gtc tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc
 Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Glu Pro Ser Thr Ala Pro Ser Thr
 807 tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct gaa ggg agc act ggc gac ttc gct ctc cca
 Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro
 873 gtt gga ctg att gtc ggt gtc aca gcc ttg ggt cta ata ata gga gtc gtc aac tgc gtc atc
 230 Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile
 939 atg acc cag gtc aaa aag aag ccc ttg tgc ctg cag aga gaa gcc aag gtc cct cac ttg cct gcc
 (Met Thr) Gln Val Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala
 1005 gat aag gcc cgg ggt aca cag ggc ccc agc cag cag cag ctc ctg atc aca ggc ccg agc tcc agc
 Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser
 1071 agc agc tcc ctg gag agc tgc gcc agt ggc ttg gac aga agg ggc ccc act cgg aac cag cca cag
 Ser Ser Ser Leu Leu Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln
 1137 gca cca ggc gtc gag gcc agt ggg gcc ggc gag gcc cgg gcc agc acc ggg agc tca gat tct tcc
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
 1203 ctt ggt gcc cat ggg acc cag gtc aat gtc acc tgc atc gtc aac gtc tgc agc agc tot gac cac
 Ala Pro Gly Val Glu Ala Ser Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Asp His
 1269 agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga ggc aca gat tcc agc ccc tgc gag tcc
 Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser
 1335 cgg aag gag cag gtc ccc ttc tcc aag gag gaa tgc gtc ttt cgg tca cag ctg gag acg cca
 384 Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
 1401 gag acc ctg ctg ggg agc acc gaa gag agc ccc ctg ccc ctt gga gtc cct gat gct ggg atg aag
 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys
 1467 ccc agt taa ccaggccggt ggggctgtg tctagaccaa ggtgggtga gccctggcag gatgacctg cgaaggggc
 439 Pro Ser End

TRANSMEMBRANE

DOMAIN

FIG. 3

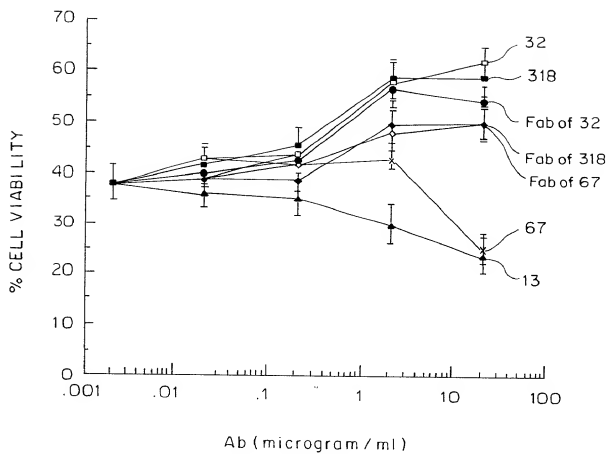


FIG. 4

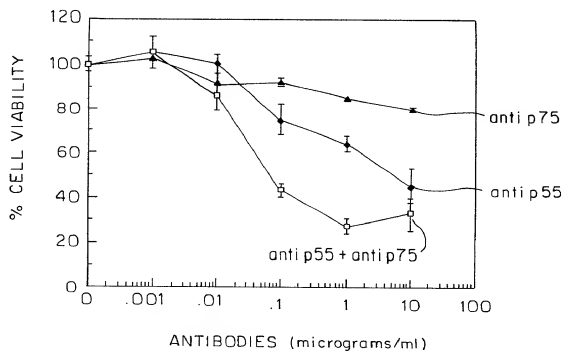


FIG. 5

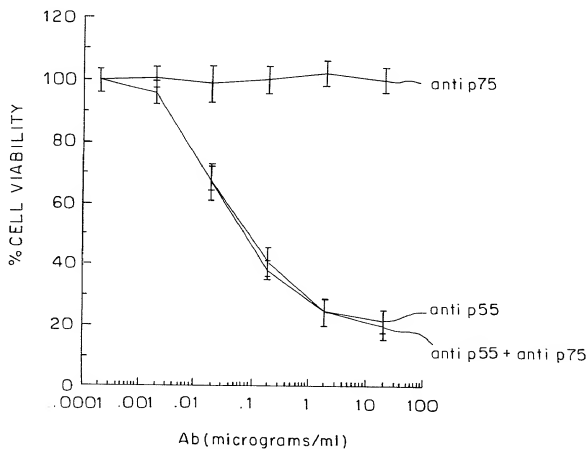


FIG. 6

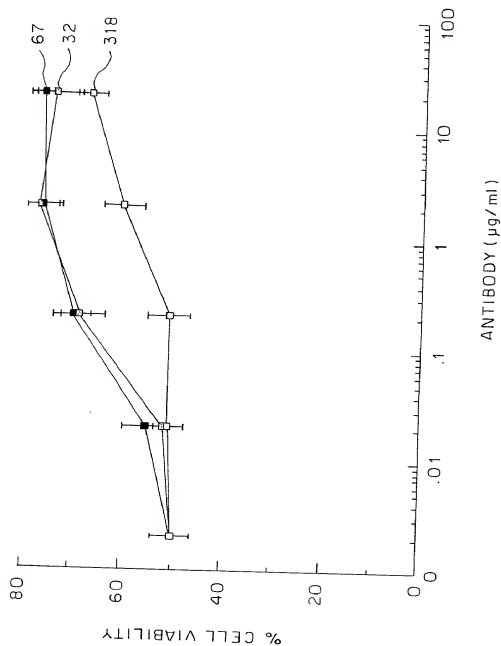


FIG. 7

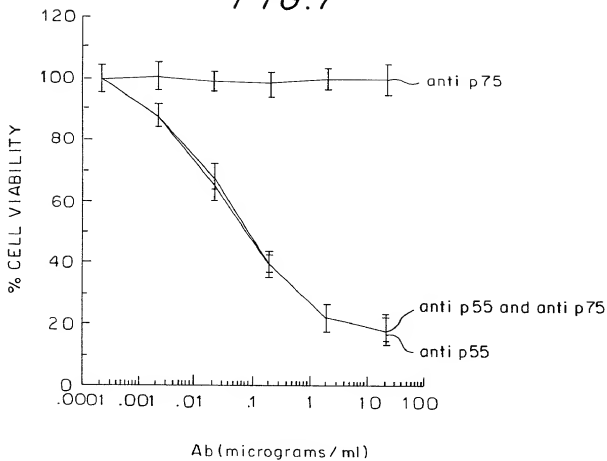


FIG. 8

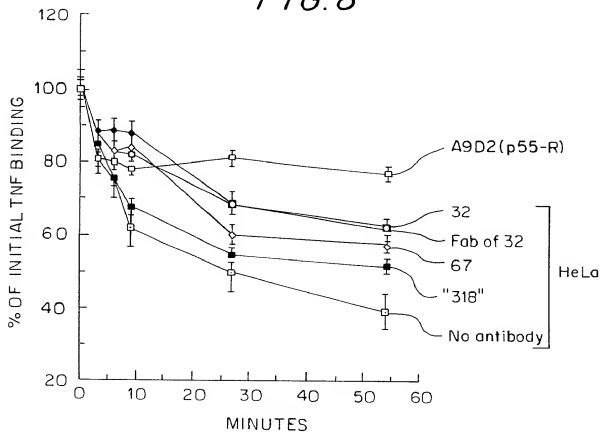


FIG.9

hu p55 TNF-R (3-42)
 hu p75 TNF-R (39-76)
 hu FAS (31-67)
 hu NGF-R (3-37)
 hu CDw40 (25-60)
 rat OX40 (25-60)

hu p55 TNF-R (43-86)
 hu p75 TNF-R (77-119)
 hu FAS (68-112)
 hu NGF-R (38-80)
 hu CDw40 (61-104)
 rat OX40 (61-104)

hu p55 TNF-R (87-126)
 hu p75 TNF-R (120-162)
 hu FAS (113-149)
 hu NGF-R (81-119)
 hu CDw40 (105-144)
 rat OX40 (105-123)

hu p55 TNF-R (127-155)
 hu p75 TNF-R (163-201)
 hu NGF-R (120-181)
 hu CDw40 (145-186)
 rat OX40 (124-164)

VCPQKXVILHPQNN-----SICCTKCHKGTLYLND-CPGEGQDTPDR
 TCRRLREYD-QTA---QMCCSKSCSPGQHAKVF-CTKTS-DATVDD
 QNLEGLH-HDGF-----CH-KPCPPEGERKARD-CTVNGDEPDIV
 ACPTGLTTHSGE-----CC-KACNLSGEGVAQP-CGA-NQTVCE
 ACREKQILINSQ-----CC-SLCQPCQKLVSD-CTEF-TETTECL
 NCVKQTYPSGHK-----CC-RECQPGHGMVSR-CDHT-RATVCH

ECESQSFATASEHHL-RHCLSL-SKCRKENGQVEITSSCTVYD-RATVCG
 SCEDSTYTQLNWV-PECLSCSRCSDD-QVETQACHRE-QNLTCT
 FCQCKEYTDKAHFSKCRRCRLCDEGHGLEVEINCHRT-QNKTQR
 PCLDSVTSSDVVSATPPCKPC-TECVGLQSHSAP-CVEA-DDAVCR
 PCGESSEFLDTWRETN-CHQH-KYCDNLLGLRVQKQKQSE-TDTTCT
 PC-EPGEPYNEAVY-DTCQKQCTQCNHRSSSELKQNCPT-EDTVCC

-CRKNQVRHYWSENLFQCFNC--SLCLHGT-VHLSQCEK-QNTVVC-
 -CRPSWICA--LSKQEGCRLCAPLRKCRPFGVARGPGET-SDVVCK
 -CRPNFFCN-STVCEHCDPC--TKCEHGLIKE-CULT-SNTK-
 -CAYGYOD--ETGRCCEAC--RVCEAGSLVFSQDCK-NTVCE
 -CEGWHC-----TSACESECVLHRSQSPGFWKQIATGV-SDTICE
 -CRPGTQP-----RQDS-----SHKLGVD-----CV

TCHAGFFLR-ENE---CVSC-SNCKKSL-----ETNK-----LC-
 PCAGTFNTTST-DICRPH-QICN---VVA-IPGNASMDAMCT
 ECPDGTYSDEAHV-DPCLPC-TVEDTEROLR-ETRW-ADAECE
 PCPVGFNSVSSAF-EKCH-TSECTKDLVQ-QAGTNKTDVVC
 PCPEGFHFGSHQ---ACRPW-TNCTLSGKQIR-HPASNSJDTVCE